



RAW SEQUENCE LISTING

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Application Serial Number: 10/526, 468
Source: PLT
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PCT

RAW SEQUENCE LISTING

DATE: 03/03/2006

PATENT APPLICATION: US/10/526,468

TIME: 12:50:19

Input Set : A:\sequence listing.txt

Output Set: N:\CRF4\03032006\J526468.raw

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3 <110> APPLICANT: Ernst-Moritz-Arndt Universitat Greifswald
5 <120> TITLE OF INVENTION: Modulation of the Synthesis of Insulin
6 <130> FILE REFERENCE: P 64322
C--> 7 <140> CURRENT APPLICATION NUMBER: US/10/526,468
C--> 7 <141> CURRENT FILING DATE: 2005-03-03
7 <160> NUMBER OF SEQ ID NOS: 12
8 <170> SOFTWARE: PatentIn version 3.1
11 <210> SEQ ID NO: 1
12 <211> LENGTH: 852
13 <212> TYPE: DNA
14 <213> ORGANISM: Homo sapiens
15 <220> FEATURE:
W--> 16 <221> NAME/KEY: Stop codon
17 <222> LOCATION: (850)..(852)
18 <223> OTHER INFORMATION: Nucleotide sequence of PDX-1
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23 cagcgaggcc cggcgccgga gttcagcgcc agccccctg cgtgcctgta catgggccgc      120
25 cagccccgcg cgccgcccgc gcaccggttc cctggcgccc tgggcgcgct ggagcagggc      180
27 agcccccccg acatctcccc gtacgaggtg cccccctcg ccgacgaccc cgcggtggcg      240
29 caccttcacc accacctccc ggctcagctc gcgtccccc acccgcccgc cgggcccttc      300
31 ccggagggag ccgagccggg cgtcctggag gagcccaacc gcgtccagct gcctttccca      360
33 tggatgaagt ctaccaaagc tcacgcgtgg aaaggccagt gggcaggcgg cgcctacgct      420
35 gcggagccgg aggagaacaa gcggacgcgc acggcctaca cgcgcgcaca gctgctagag      480
37 ctggagaagg agttcctatt caacaagtat atctcacggc cgcgccgggt ggagctggct      540
39 gtcagtgtga acttgaccga gagacacatc aagatctggt tccaaaaccg ccgcatgaag      600
41 tggaaaaagg aggaggacaa gaagcgcggc ggccggacag ctgtcggggg tggcggggtc      660
43 gcggagcctg agcaggactg cgccgtgacc tccggcgagg agcttctggc gctgccgccg      720
45 ccgccgcccc ccggaggtgc tgtgccgccc gctgcccccg ttgccgcccg agagggccgc      780
47 ctgccgcctg gccttagcgc gtcgccacag ccctccagcg tcgcgcctcg gcggccgcag      840
49 gaaccacgat ga                                         852
66 <210> SEQ ID NO: 2
67 <211> LENGTH: 283
68 <212> TYPE: PRT
69 <213> ORGANISM: Homo sapiens
71 <223> OTHER INFORMATION: Amino acid sequence of PDX-1
73 <400> SEQUENCE: 2
74 Met Asn Gly Glu Glu Gln Tyr Tyr Ala Ala Thr Gln Leu Tyr Lys Asp
75 1          5          10          15
78 Pro Cys Ala Phe Gln Arg Gly Pro Ala Pro Glu Phe Ser Ala Ser Pro
79          20          25          30
82 Pro Ala Cys Leu Tyr Met Gly Arg Gln Pro Pro Pro Pro Pro His
83          35          40          45

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86 Pro Phe Pro Gly Ala Leu Gly Ala Leu Glu Gln Gly Ser Pro Pro Asp
87      50                      55                      60
90 Ile Ser Pro Tyr Glu Val Pro Pro Leu Ala Asp Asp Pro Ala Val Ala
91 65                      70                      75                      80
94 His Leu His His His Leu Pro Ala Gln Leu Ala Leu Pro His Pro Pro
95                      85                      90                      95
98 Ala Gly Pro Phe Pro Glu Gly Ala Glu Pro Gly Val Leu Glu Glu Pro
99                      100                      105                      110
102 Asn Arg Val Gln Leu Pro Phe Pro Trp Met Lys Ser Thr Lys Ala His
103                      115                      120                      125
106 Ala Trp Lys Gly Gln Trp Ala Gly Gly Ala Tyr Ala Ala Glu Pro Glu
107      130                      135                      140
110 Glu Asn Lys Arg Thr Arg Thr Ala Tyr Thr Arg Ala Gln Leu Leu Glu
111 145                      150                      155                      160
114 Leu Glu Lys Glu Phe Leu Phe Asn Lys Tyr Ile Ser Arg Pro Arg Arg
115                      165                      170                      175
118 Val Glu Leu Ala Val Met Leu Asn Leu Thr Glu Arg His Ile Lys Ile
119                      180                      185                      190
122 Trp Phe Gln Asn Arg Arg Met Lys Trp Lys Lys Glu Glu Asp Lys Lys
123                      195                      200                      205
127 Arg Gly Gly Gly Thr Ala Val Gly Gly Gly Gly Val Ala Glu Pro Glu
128      210                      215                      220
131 Gln Asp Cys Ala Val Thr Ser Gly Glu Glu Leu Leu Ala Leu Pro Pro
132 225                      230                      235                      240
135 Pro Pro Pro Pro Gly Gly Ala Val Pro Pro Ala Ala Pro Val Ala Ala
136                      245                      250                      255
139 Arg Glu Gly Arg Leu Pro Pro Gly Leu Ser Ala Ser Pro Gln Pro Ser
140                      260                      265                      270
143 Ser Val Ala Pro Arg Arg Pro Gln Glu Pro Arg
144      275                      280

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149 <210> SEQ ID NO: 3

150 <211> LENGTH: 1182

151 <212> TYPE: DNA

152 <213> ORGANISM: Homo sapiens

153 <220> FEATURE:

W--> 154 <221> NAME/KEY: Stop codon

155 <222> LOCATION: (1080)..(1082)

156 <223> OTHER INFORMATION: Nucleotide sequence of CK II alpha subunit

158 <400> SEQUENCE: 3

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159 atgtcgggac ccgtgccaaag cagggccaga gtttacacag atgttaatac acacagacct      60
161 cgagaataact gggattacga gtcacatgtg gtggaatggg gaaatcaaga tgactaccag      120
163 ctggttcgaa aattaggccg aggtaaatac agtgaagtat ttgaagccat caacatcaca      180
165 aataatgaaa aagttgttgt taaaattctc aagccagtaa aaaagaagaa aattaagcgt      240
167 gaaataaaga ttttggagaa tttgagagga ggtcccaaca tcatcacact ggcagacatt      300
169 gtaaaaagacc ctgtgtcacg aacccccgcc ttggtttttg aacacgtaaa caacacagac      360
171 ttcaagcaat tgtaccagac gttaacagac tatgatattc gattttacat gtatgagatt      420
173 ctgaaggccc tggattattg tcacagcatg ggaattatgc acagagatgt caagccccat      480
175 aatgtcatga ttgatcatga gcacagaaag ctacgactaa tagactgggg tttggctgag      540
177 ttttatcatc ctggccaaga atataatgtc cgagtttgctt cccgatactt caaaggtcct      600

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179 gagctacttg tagactatca gatgtacgat tatagtttgg atatgtggag tttgggttgt      660
181 atgctggcaa gtatgatctt tcggaaggag ccatttttcc atggacatga caattatgat      720
183 cagtttggtga ggatagccaa ggttctgggg acagaagatt tatatgacta tattgacaaa      780
185 tacaacattg aattagatcc acgtttcaat gatatcttgg gcagacactc tcgaaagcga      840
187 tgggaacgct ttgtccacag tgaaaatcag caccttgtca gccctgaggc cttggatttc      900
189 ctggacaaac tgctgcgata tgaccaccag tcacggctta ctgcaagaga ggcaatggag      960
191 cacccttatt tctacactgt tgtgaaggac caggctcgaa tgggttcacg tagcatgcca     1020
193 gggggcagta cgcccgtcag cagcgccaat atgatgtcag ggatttcttc agtgccaacc     1080
195 ccttcacccc ttggacctct ggcaggctca ccagtgattg ctgctgccaa ccccttggg      1140
197 atgcctgttc cagctgccgc tggcgctcag cagtaacggc cc                        1182
202 <210> SEQ ID NO: 4
203 <211> LENGTH: 391
204 <212> TYPE: PRT
205 <213> ORGANISM: Homo sapiens
207 <223> OTHER INFORMATION: Amino acid sequence of CKII alpha subunit
209 <400> SEQUENCE: 4
210 Met Ser Gly Pro Val Pro Ser Arg Ala Arg Val Tyr Thr Asp Val Asn
211 1 5 10 15
214 Thr His Arg Pro Arg Glu Tyr Trp Asp Tyr Glu Ser His Val Val Glu
215 20 25 30
218 Trp Gly Asn Gln Asp Asp Tyr Gln Leu Val Arg Lys Leu Gly Arg Gly
219 35 40 45
222 Lys Tyr Ser Glu Val Phe Glu Ala Ile Asn Ile Thr Asn Asn Glu Lys
223 50 55 60
226 Val Val Val Lys Ile Leu Lys Pro Val Lys Lys Lys Lys Ile Lys Arg
227 65 70 75 80
230 Glu Ile Lys Ile Leu Glu Asn Leu Arg Gly Gly Pro Asn Ile Ile Thr
231 85 90 95
234 Leu Ala Asp Ile Val Lys Asp Pro Val Ser Arg Thr Pro Ala Leu Val
235 100 105 110
238 Phe Glu His Val Asn Asn Thr Asp Phe Lys Gln Leu Tyr Gln Thr Leu
239 115 120 125
242 Thr Asp Tyr Asp Ile Arg Phe Tyr Met Tyr Glu Ile Leu Lys Ala Leu
243 130 135 140
246 Asp Tyr Cys His Ser Met Gly Ile Met His Arg Asp Val Lys Pro His
247 145 150 155 160
250 Asn Val Met Ile Asp His Glu His Arg Lys Leu Arg Leu Ile Asp Trp
251 165 170 175
257 Gly Leu Ala Glu Phe Tyr His Pro Gly Gln Glu Tyr Asn Val Arg Val
258 180 185 190
261 Ala Ser Arg Tyr Phe Lys Gly Pro Glu Leu Leu Val Asp Tyr Gln Met
262 195 200 205
265 Tyr Asp Tyr Ser Leu Asp Met Trp Ser Leu Gly Cys Met Leu Ala Ser
266 210 215 220
269 Met Ile Phe Arg Lys Glu Pro Phe Phe His Gly His Asp Asn Tyr Asp
270 225 230 235 240
273 Gln Leu Val Arg Ile Ala Lys Val Leu Gly Thr Glu Asp Leu Tyr Asp
274 245 250 255
277 Tyr Ile Asp Lys Tyr Asn Ile Glu Leu Asp Pro Arg Phe Asn Asp Ile

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278          260          265          270
281 Leu Gly Arg His Ser Arg Lys Arg Trp Glu Arg Phe Val His Ser Glu
282          275          280          285
285 Asn Gln His Leu Val Ser Pro Glu Ala Leu Asp Phe Leu Asp Lys Leu
286          290          295          300
289 Leu Arg Tyr Asp His Gln Ser Arg Leu Thr Ala Arg Glu Ala Met Glu
290 305          310          315          320
293 His Pro Tyr Phe Tyr Thr Val Val Lys Asp Gln Ala Arg Met Gly Ser
294          325          330          335
297 Ser Ser Met Pro Gly Gly Ser Thr Pro Val Ser Ser Ala Asn Met Met
298          340          345          350
301 Ser Gly Ile Ser Ser Val Pro Thr Pro Ser Pro Leu Gly Pro Leu Ala
302          355          360          365
305 Gly Ser Pro Val Ile Ala Ala Asn Pro Leu Gly Met Pro Val Pro
306          370          375          380
309 Ala Ala Ala Gly Ala Gln Gln
310 385          390

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320 <210> SEQ ID NO: 5

321 <211> LENGTH: 1053

322 <212> TYPE: DNA

323 <213> ORGANISM: Homo sapiens

325 <220> FEATURE:

W--> 326 <221> NAME/KEY: Stop codon

327 <222> LOCATION: (1051)..(1053)

328 <223> OTHER INFORMATION: Nucleotide sequence of CKII alpha? subunit

330 <400> SEQUENCE: 5

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331 atgcccgccc cggccgcggg cagcagggcc cgggtctacg ccgaggtgaa cagtctgagg      60
333 agccgcgagt actgggacta cgaggctcac gtcccagact ggggtaatca agatgattac      120
335 caactgggtt gaaaacttgg tcggggaaaa tatagtgaag tatttgaggc cattaatatc      180
337 accaacaatg agagagtggg tgtaaaaatc ctgaagccag tgaagaaaaa gaagataaaa      240
339 cgagaggtta agattctgga gaaccttcgt ggtggaacaa atatcattaa gctgattgac      300
341 actgtaaagg acccctgtgc aaagacacca gctttggtat ttgaatatat caataatata      360
343 gattttaagc aactctacca gatcctgaca gactttgata tccggtttta tatgtatgaa      420
345 ctacttaaaag ctctggatta ctgccacagc aaggggaatca tgcacagggg tgtgaaacct      480
347 cacaatgtca tgatagatca ccaacagaaa aagctgcgac tgatagattg ggggtctggca      540
349 gaattctatc atcctgctca ggagtacaat gttcgtgtag cctcaaggta cttcaagggg      600
351 ccagagctcc tcgtggacta tcagatgtat gattatagct tggacatgtg gagtttgggc      660
353 tgtatgtag caagcatgat ctttcgaagg gaaccattct tccatggaca ggacaactat      720
355 gaccagcttg ttcgcattgc caaggttctg ggtacagaag aactgtatgg gtatctgaag      780
357 aagtatcaca tagacctaga tccacacttc aacgatatcc tgggacaaca ttcacggaaa      840
359 cgctgggaaa actttatcca tagtgagaac agacaccttg tcagccctga ggccctagat      900
361 cttctggaca aacttctgcg atacgaccat caacagagac tgactgcaa agaggccatg      960
363 gagcacccat acttctaccc tgtggtgaag gagcagtcgc agccttgtgc agacaatgct     1020
365 gtgctttcca gtggtctcac ggcagcacga tga                                1053

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370 <210> SEQ ID NO: 6

371 <211> LENGTH: 350

372 <212> TYPE: PRT

373 <213> ORGANISM: Homo sapiens

374 <223> OTHER INFORMATION: Amino acid sequence of CK II alpha? subunit

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378 <400> SEQUENCE: 6
379 Met Pro Gly Pro Ala Ala Gly Ser Arg Ala Arg Val Tyr Ala Glu Val
380 1 5 10 15
383 Asn Ser Leu Arg Ser Arg Glu Tyr Trp Asp Tyr Glu Ala His Val Pro
384 20 25 30
387 Ser Trp Gly Asn Gln Asp Asp Tyr Gln Leu Val Arg Lys Leu Gly Arg
388 35 40 45
391 Gly Lys Tyr Ser Glu Val Phe Glu Ala Ile Asn Ile Thr Asn Asn Glu
392 50 55 60
395 Arg Val Val Val Lys Ile Leu Lys Pro Val Lys Lys Lys Lys Ile Lys
396 65 70 75 80
399 Arg Glu Val Lys Ile Leu Glu Asn Leu Arg Gly Gly Thr Asn Ile Ile
400 85 90 95
403 Lys Leu Ile Asp Thr Val Lys Asp Pro Val Ser Lys Thr Pro Ala Leu
404 100 105 110
407 Val Phe Glu Tyr Ile Asn Asn Thr Asp Phe Lys Gln Leu Tyr Gln Ile
408 115 120 125
411 Leu Thr Asp Phe Asp Ile Arg Phe Tyr Met Tyr Glu Leu Leu Lys Ala
412 130 135 140
415 Leu Asp Tyr Cys His Ser Lys Gly Ile Met His Arg Asp Val Lys Pro
416 145 150 155 160
419 His Asn Val Met Ile Asp His Gln Gln Lys Lys Leu Arg Leu Ile Asp
420 165 170 175
423 Trp Gly Leu Ala Glu Phe Tyr His Pro Ala Gln Glu Tyr Asn Val Arg
424 180 185 190
427 Val Ala Ser Arg Tyr Phe Lys Gly Pro Glu Leu Leu Val Asp Tyr Gln
428 195 200 205
431 Met Tyr Asp Tyr Ser Leu Asp Met Trp Ser Leu Gly Cys Met Leu Ala
432 210 215 220
435 Ser Met Ile Phe Arg Arg Glu Pro Phe Phe His Gly Gln Asp Asn Tyr
436 225 230 235 240
439 Asp Gln Leu Val Arg Ile Ala Lys Val Leu Gly Thr Glu Glu Leu Tyr
440 245 250 255
443 Gly Tyr Leu Lys Lys Tyr His Ile Asp Leu Asp Pro His Phe Asn Asp
444 260 265 270
447 Ile Leu Gly Gln His Ser Arg Lys Arg Trp Glu Asn Phe Ile His Ser
448 275 280 285
451 Glu Asn Arg His Leu Val Ser Pro Glu Ala Leu Asp Leu Leu Asp Lys
452 290 295 300
456 Leu Leu Arg Tyr Asp His Gln Gln Arg Leu Thr Ala Lys Glu Ala Met
457 305 310 315 320
460 Glu His Pro Tyr Phe Tyr Pro Val Val Lys Glu Gln Ser Gln Pro Cys
461 325 330 335
465 Ala Asp Asn Ala Val Leu Ser Ser Gly Leu Thr Ala Ala Arg
466 340 345 350
471 <210> SEQ ID NO: 7
472 <211> LENGTH: 648
473 <212> TYPE: DNA
474 <213> ORGANISM: Homo sapiens

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VERIFICATION SUMMARYPATENT APPLICATION: **US/10/526,468**

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L:7 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:16 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:154 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:326 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:477 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:585 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9
L:704 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11